

REMARKS

The information contained in the computer readable form of Application No. 09/686,020 was prepared through the use of the software program "PatentIn" and was identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 25 of page 2 has been amended as follows:

In a related aspect, the invention provides an isolated polynucleotide that encodes, or is complementary to a sequence that encodes, the CCX CKR polypeptide. In some embodiments the polynucleotide has at least 10, 15, 25, 50 or 100 contiguous bases identical or exactly complementary to SEQ ID NO:1. In various embodiments, the polynucleotide is the full-length sequence of SEQ ID NO:1, encodes a CCX CKR polypeptide of the invention (e.g., having the sequence of SEQ ID NO:2 ~~SEQ ID:2~~ or a fragment thereof), or selectively hybridizes under high stringent hybridization conditions to a polynucleotide sequence of SEQ ID NO:1. The polynucleotide of the invention may be operably linked to a promoter. The invention provides recombinant vector (e.g., an expression vector) expressing the CCX CKR polypeptides of the invention. In one aspect, the invention provides a polynucleotide having sequence encoding a polypeptide that has an activity (e.g., a chemokine binding activity) of a CCX CKR polypeptide and which is (a) a polynucleotide having the sequence of SEQ ID NO:1 or SEQ ID NO:3 ~~SEQ ID NO:3~~; or (b) a polynucleotide which hybridizes under stringent conditions to (a); or (c) a polynucleotide sequence which is degenerate as a result of the genetic code to the sequences defined in (a) or (b).

Paragraph beginning at line 3 of page 5 has been amended as follows:

Figure 1 shows the nucleotide sequence for a human CCX CKR (SEQ ID NO:1) (~~SEQ ID NO:1~~) and the predicted amino acid sequence of the human CCX CKR polypeptide (SEQ ID NOS:2 and 12-14) (~~SEQ ID NO:2~~).

Paragraph beginning at line 7 of page 5 has been amended as follows:

Figure 2 shows the CCX CKR sequence aligned with those of other chemokine receptors, the expression pattern of CCX CKR RNA, and generation of a stable cell line expressing CCX CKR. Figure 2A shows sequence homology of the CCX CKR coding region (SEQ ID NO:2) with other chemokine receptors (SEQ ID NOS:6-9). Figure 2B shows cells and tissues expressing CCX CKR RNA, as analyzed by RT-PCR of cytoplasmic RNA from cultured primary cells and whole tissues from various organs as indicated. Figure 2C shows a population of transfected HEK-293 cells stably expressing CCX CKR protein containing an N-terminal Flag epitope, comparing intensity of anti-Flag mAb staining relative to wild type HEK293 cells.

Paragraph beginning at line 13 of page 6 has been amended as follows:

Figure 5 shows DNA sequence 5' to the translation start site of the CCX CKR gene (SEQ ID NOS:10 and 11), as determined from a genomic clone.



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SEQUENCE LISTING

<110> Rosling, Jennifa
Dairaghi, Daniel J.
Hanley, Michael
Miao, Zhenhua
Schall, Thomas J.
ChemoCentryx, Inc.

<120> Chemokine Receptor

<130> 019934-000710US

<140> US 09/686,020
<141> 2000-10-10

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<170> PatentIn Ver. 2.1

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<211> 1147
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1053)

<220>
<223> chemokine receptor (CCX CKR)

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Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
1 5 10 15

gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc 96
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
20 25 30

aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc 144
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
35 40 45

as

aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala	
50 55 60	
att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile	
65 70 75 80	
ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe	
85 90 95	
tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys	
100 105 110	
aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln	
115 120 125	
ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc	432
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val	
130 135 140	
ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt	480
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys	
145 150 155 160	
gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr	
165 170 175	
aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu	
180 185 190	
gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly	
195 200 205	
ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca	672
Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala	
210 215 220	
agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa	720
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys	
225 230 235 240	
gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat	768
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr	
245 250 255	
aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc	816
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile	
260 265 270	
acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca	864
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr	
275 280 285	

95
cont

gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt 912
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
 290 295 300

 ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa 960
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
 305 310 315 320

 tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt 1008
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
 325 330 335

 gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa 1053
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
 340 345 350

 aggtaaaact gctctgcctt ttgcttggat acatatgaat gatgctttcc cctcaaataa 1113
 aacatctgcc ttattctgaa aaaaaaaaaa aaam 1147

<210> 2
 <211> 350
 <212> PRT
 <213> Homo sapiens
 <223> chemokine receptor (CCX CKR)

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 1 5 10 15
 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
 20 25 30
 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45
 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
 50 55 60
 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
 65 70 75 80
 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe
 85 90 95
 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
 100 105 110
 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
 115 120 125
 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
 130 135 140
 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
 145 150 155 160
 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
 165 170 175
 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
 180 185 190
 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
 195 200 205
 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
 210 215 220
 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
 225 230 235 240
 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
 245 250 255

Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
 260 265 270
 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
 275 280 285
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
 290 295 300
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
 305 310 315 320
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
 325 330 335
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
 340 345 350

<210> 3
 <211> 1147
 <212> DNA
 <213> Homo sapiens

<220>
 <223> chemokine receptor (variant)

<400> 3
 atggcctttgg aacagaacca gtcaacagat tattattatg aggaaagtga aatgaatggc 60
 actgatgact acagtcagta tgaactgac tgtatcaaag aagatgtcag agaatttgcc 120
 aaagttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
 ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcctttttg ggctgttaat 300
 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
 ctaaaactttg tctctggaat gcagtttctg gcttgtatca gcatagacag atatgtggca 420
 gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480
 gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaagtac 540
 aatgttaggt gcattcccat tttccccgc aacttaggaa catcaatgaa agcattgatt 600
 caaatgctag agatctgcat tggatttgta gtacccttct ttattatggg ggtgtgctac 660
 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
 ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
 atggacatcg ccatccaagt cacagaaagc atcgactctt ttcacagctg cctcaaccca 900
 atcctttatg tttttatggg agcatcttct aaaaactacg ttatgaaagt ggccaagaaa 960
 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggg 1020
 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
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 aaaaaam 1147

<210> 4
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 4
 aatttgctg tagcagattt actcc

25

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 5
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19

<210> 6
 <211> 369
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chemokine receptor (CCR9)

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 Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr Val Asn Phe Asn
 20 25 30
 Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser
 35 40 45
 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
 50 55 60
 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
 65 70 75 80
 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
 85 90 95
 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Asp Gln Trp
 100 105 110
 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
 115 120 125
 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
 130 135 140
 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
 145 150 155 160
 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
 165 170 175
 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
 180 185 190
 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
 195 200 205

95
 cont

Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
 210 215 220
 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
 225 230 235 240
 Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr
 245 250 255
 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
 260 265 270
 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn
 275 280 285
 Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val Thr Gln Thr
 290 295 300
 Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Val
 305 310 315 320
 Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys Asn Leu Gly
 325 330 335
 Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg Glu Gly Ser
 340 345 350
 Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly Ala Leu Ser
 355 360 365
 Leu

<210> 7
 <211> 378
 <212> PRT
 <213> Homo sapiens

<220>
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 20 25 30
 Ile Gly Asp Asn Thr Thr Val Asp Tyr Thr Leu Phe Glu Ser Leu Cys
 35 40 45
 Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
 50 55 60
 Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
 65 70 75 80
 Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
 85 90 95

Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro
 100 105 110
 Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe
 115 120 125
 Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met
 130 135 140
 Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln
 145 150 155 160
 Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys
 165 170 175
 Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile Pro
 180 185 190
 Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met
 195 200 205
 Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln
 210 215 220
 Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser
 225 230 235 240
 Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe
 245 250 255
 Glu Arg Asn Lys Ala Ile Lys Val Ile Ile Ala Val Val Val Val Phe
 260 265 270
 Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val
 275 280 285
 Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu
 290 295 300
 Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
 305 310 315 320
 Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
 325 330 335
 Ile Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu
 340 345 350
 Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser Val
 355 360 365
 Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro
 370 375

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

<220>
<223> chemokine receptor (CCR6)

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20 25 30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
35 40 45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
50 55 60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65 70 75 80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
85 90 95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
100 105 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
115 120 125
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
130 135 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145 150 155 160
Leu Pro Arg Thr Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
165 170 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180 185 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
195 200 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
210 215 220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225 230 235 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
245 250 255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
260 265 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
275 280 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
290 295 300

25
cont

Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
 340 345 350
 Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
 355 360 365
 Ala Ser Ser Phe Thr Met
 370

<210> 9
 <211> 342
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chemokine receptor (STRL33)

<400> 9
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 Asp Ser Ser Gln Glu Glu His Gln Asp Phe Leu Gln Phe Ser Lys Val
 20 25 30
 Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly
 35 40 45
 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
 50 55 60
 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
 65 70 75 80
 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
 85 90 95
 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
 100 105 110
 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
 115 120 125
 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
 130 135 140
 Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
 145 150 155 160
 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
 165 170 175
 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
 180 185 190

Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
195 200 205

Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
210 215 220

Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
225 230 235 240

Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
245 250 255

His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
260 265 270

Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
275 280 285

Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
290 295 300

Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
305 310 315 320

Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala
325 330 335

Thr Ser Met Phe Gln Leu
340

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<211> 740
<212> DNA
<213> Homo sapiens

<220>
<223> region containing residues 5' to the translation
start site of CCX CKR

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tatttaactt atttaaatta aattttataaa taacatcaaa ataaaaaata aatttaattt 120
aaataaacca agtaatttgc tattttcgtt tttattcaat ttgtttaga tatactttta 180
cgattcacaa aattatgtat gtaaagatta taacactatt tattcttttt agttaaaatc 240
taattaaatt ttcataattt aaaaatcatt tttacataaa agtcttcact tttatttagg 300
atttaaatgat taagaaaatt ctccagggca ttatgtttat tgtcctgttc aaatccaagc 360
tctttcacac agaattgtac aagcaaagtt tgagtaacta atcttggggc catattccaa 420
tgtggctccc attaaagcat ttcaaagagt gctagattca ggctcacata tgttacagca 480
acaggctata ctctagggaa agaacaaaac agcttgatag aaactgtgtg cttttaagca 540
tatttagaca aatatctatc ctgtattctc tttgccatct agattggagc catggctttg 600
gaacagaacc gtcaacagat tattattatg aggagaagtg aaatgaatgg cctgatgact 660
acagtcagta tgaactgatc tgttcagaga agagacagag gatatgcaca gggttgctcc 720
ctgtattgct caccatagag 740

<210> 11
<211> 347
<212> DNA
<213> Homo sapiens

<220>

<223> selected portion of SEQ ID NO:1

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aaagttttcc tccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcctttttg ggctgttaat 300
gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttc 347
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<210> 12

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<223> translation of non-coding region of SEQ ID NO:1

<400> 12

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Asn Cys Ser Ala Phe Cys Leu Asp Thr Tyr Glu
  1              5              10
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<210> 13

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<223> translation of non-coding region of SEQ ID NO:1

<400> 13

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Cys Phe Pro Leu Lys
  1              5
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<210> 14

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<223> translation of non-coding region of SEQ ID NO:1

<400> 14

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Asn Ile Cys Leu Ile Leu Lys Lys Lys Lys Lys
  1              5              10
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